SEQUENCE LISTING

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<110>   Myers, Alan M.
        James, Martha G.
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         <213>     artificial sequence
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                   site in the left arm in (gt11 phage DNA used to
                   amplify cDNA inserts
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                   site in the LacZ' region in the right arm in (gt11
                   phage DNA used to amplify cDNA inserts.
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         <210>     8
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          <222>   REPEAT
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                  residue sequence of SBE-repeat in DU1.
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Asp Gln Ser Ile Val Gly
 1               5


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          <212>   PRT
          <213>   maize
          <220>
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          <223>   Four residue sequence of second half-repeat of
                  ten residue SBE-repeat sequence in DU1.
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Ser His Lys Gln
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          <212>   PRT
          <213>   unknown
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          <222>   REPEAT
          <223>   M-box sequence in SBEI enzyme.
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Asp Gln Ala Leu Val Gly
 1               5


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          <213>   maize
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Gly Pro Val Leu Ile Phe Arg Pro Thr Val Ala Gly Gly Gly Gly
                20                  25                  30

Gly Thr Gln Ser Leu Leu Arg Thr Thr Arg Phe Ala Arg Arg Arg
                35                  40                  45

Val Ile Arg Cys Val Val Ala Ser Pro Gly Cys Pro Asn Arg Lys
                50                  55                  60

Ser Arg Thr Ala Ser Pro Asn Val Lys Val Ala Ala Tyr Ser Asn
                65                  70                  75

Tyr Ala Pro Arg Leu Leu Val Glu Ser Ser Ser Lys Lys Ser Glu
                80                  85                  90


His His Asp Ser Ser Arg His Arg Glu Glu Thr Ile Asp Thr Tyr
                95                  100                 105


Asn Gly Leu Ser Gly Ser Asp Ala Ala Glu Leu Thr Ser Asn Arg
                110                 115                 120
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Asp Val Glu Ile Glu Val Asp Leu Gln His Ile Ser Glu Glu Glu
            125                 130                 135

Leu Pro Gly Lys Val Ser Ile Asn Ala Ser Leu Gly Glu Met Glu
                140                 145                 150

Thr Val Asp Glu Ala Glu Val Glu Glu Asp Lys Phe Glu Val Asp
                155                 160                 165

Thr Ser Gly Ile Val Leu Arg Asn Val Ala Val Arg Glu Val Asp
                170                 175                 180

Pro Lys Asp Glu His Asn Ala Lys Asp Val Phe Val Val Asp Ser
                185                 190                 195

Ser Gly Thr Ala Pro Asp Asn Ala Ala Val Glu Glu Val Val Asp
                200                 205                 210

Glu Ala Glu Val Glu Glu Asp Met Val Asp Val Asp Ile Leu Gly
                215                 220                 225

Leu Asp Leu Asn Asn Ala Thr Ile Glu Glu Ile Asp Leu Met Glu
                230                 235                 240

Glu Ala Leu Leu Glu Asn Phe Asp Val Asp Ser Pro Gly Asn Ala
                245                 250                 255

Ser Ser Gly Arg Thr Tyr Gly Gly Val Asp Glu Leu Gly Glu Leu
                260                 265                 270


Pro Ser Thr Ser Val Asp Cys Ile Ala Ile Asn Gly Lys Arg Arg
                275                 280                 285

Ser Leu Lys Pro Lys Pro Leu Pro Ile Val Arg Phe Gln Glu Gln
                290                 295                 300

Glu Gln Ile Val Leu Ser Ile Val Asp Glu Glu Gly Leu Ile Ala
                305                 310                 315

Ser Ser Cys Glu Glu Gly Gln Pro Val Val Asp Tyr Asp Lys Gln
                320                 325                 330

Glu Glu Asn Ser Thr Ala Phe Asp Glu Gln Lys Gln Leu Thr Asp
                335                 340                 345

Asp Phe Pro Glu Glu Gly Ile Ser Ile Val His Phe Pro Glu Pro
                350                 355                 360

Asn Asn Asp Ile Val Gly Ser Ser Lys Phe Leu Glu Gln Lys Gln
                365                 370                 375

Glu Leu Asp Gly Ser Tyr Lys Gln Asp Arg Ser Thr Thr Gly Leu
                380                 385                 390

His Glu Gln Asp Gln Ser Val Val Ser Ser His Gly Gln Asp Lys
                395                 400                 405

Ser Ile Val Gly Val Pro Gln Gln Ile Gln Tyr Asn Asp Gln Ser
                410                 415                 420

Ile Ala Gly Ser His Arg Gln Asp Gln Ser Ile Ala Gly Ala Pro
                425                 430                 435

Glu Gln Ile Gln Ser Val Ala Gly Tyr Ile Lys Pro Asn Gln Ser
                440                 445                 450
```

```
Ile Val Gly Ser Cys Lys Gln His Glu Leu Ile Ile Pro Glu Pro
              455             460             465

Lys Lys Ile Glu Ser Ile Ile Ser Tyr Asn Glu Ile Asp Gln Ser
              470             475             480

Ile Val Gly Ser His Lys Gln Asp Lys Ser Val Val Ser Val Pro
              485             490             495

Glu Gln Ile Gln Ser Ile Val Ser His Ser Lys Pro Asn Gln Ser
              500             505             510

Thr Val Asp Ser Tyr Arg Gln Ala Glu Ser Ile Ile Gly Val Pro
              515             520             525

Glu Lys Val Gln Ser Ile Thr Ser Tyr Asp Lys Leu Asp Gln Ser
              530             535             540

Ile Val Gly Ser Leu Lys Gln Asp Glu Pro Ile Ile Ser Val Pro
              545             550             555

Glu Lys Ile Gln Ser Ile Val His Tyr Thr Lys Pro Asn Gln Ser
              560             565             570

Ile Val Gly Leu Pro Lys Gln Gln Gln Ser Ile Val His Ile Val
              575             580             585

Glu Pro Lys Gln Ser Ile Asp Gly Phe Pro Lys Gln Asp Leu Ser
              590             595             600

Ile Val Gly Ile Ser Asn Glu Phe Gln Thr Lys Gln Leu Ala Thr
              605             610             615

Val Gly Thr His Asp Gly Leu Leu Met Lys Gly Val Glu Ala Lys
              620             625             630


Glu Thr Ser Gln Lys Thr Glu Gly Asp Thr Leu Gln Ala Thr Phe
              635             640             645

Asn Val Asp Asn Leu Ser Gln Lys Gln Glu Gly Leu Thr Lys Glu
              650             655             660

Ala Asp Glu Ile Thr Ile Ile Glu Lys Ile Asn Asp Glu Asp Leu
              665             670             675

Val Met Ile Glu Glu Gln Lys Ser Ile Ala Met Asn Glu Glu Gln
              680             685             690

Thr Ile Val Thr Glu Glu Asp Ile Pro Met Ala Lys Val Glu Ile
              695             700             705

Gly Ile Asp Lys Ala Lys Phe Leu His Leu Leu Ser Glu Glu Glu
              710             715             720

Ser Ser Trp Asp Glu Asn Glu Val Gly Ile Ile Glu Ala Asp Glu
              725             730             735

Gln Tyr Glu Val Asp Glu Thr Ser Met Ser Thr Glu Gln Asp Ile
              740             745             750

Gln Glu Ser Pro Asn Asp Asp Leu Asp Pro Gln Ala Leu Trp Ser
              755             760             765

Met Leu Gln Glu Leu Ala Glu Lys Asn Tyr Ser Leu Gly Asn Lys
```

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Leu Tyr Phe Asn Arg Asp Leu Ser Ala Ala Asn Glu Pro Asp
            800             805             810


Val Leu Ile Lys Gly Ala Phe Asn Gly Trp Lys Trp Arg Phe Phe
            815             820             825
Thr Glu Lys Leu His Lys Ser Glu Leu Ala Gly Asp Trp Trp Cys
            830             835             840
Cys Lys Leu Tyr Ile Pro Lys Gln Ala Tyr Arg Met Asp Phe Val
            845             850             855
Phe Phe Asn Gly His Thr Val Tyr Glu Asn Asn Asn Asn Asn Asp
            860             865             870
Phe Val Ile Gln Ile Glu Ser Thr Met Asp Glu Asn Leu Phe Glu
            875             880             885
Asp Phe Leu Ala Glu Glu Lys Gln Arg Glu Leu Glu Asn Leu Ala
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Asn Glu Glu Ala Glu Arg Arg Arg Gln Thr Asp Glu Gln Arg Arg
            905             910             915
Met Glu Glu Glu Arg Ala Ala Asp Lys Ala Asp Arg Val Gln Ala
            920             925             930
Lys Val Glu Val Glu Thr Lys Lys Asn Lys Leu Cys Asn Val Leu
            935             940             945
Gly Leu Ala Arg Ala Pro Val Asp Asn Leu Trp Tyr Ile Glu Pro
            950             955             960
Ile Thr Thr Gly Gln Glu Ala Thr Val Arg Leu Tyr Tyr Asn Ile
            965             970             975
Asn Ser Arg Pro Leu Val His Ser Thr Glu Ile Trp Met His Gly
            980             985             990


Gly Tyr Asn Asn Trp Ile Asp Gly Leu Ser Phe Ala Glu Arg Leu
            995             1000            1005
Val His His His Asp Lys Asp Cys Asp Trp Trp Phe Ala Asp Val
            1010            1015            1020
Val Val Pro Glu Arg Thr Tyr Val Leu Asp Trp Val Phe Ala Asp
            1025            1030            1035
Gly Pro Pro Gly Ser Ala Arg Asn Tyr Asp Asn Asn Gly Gly His
            1040            1045            1050
Asp Phe His Ala Thr Leu Pro Asn Asn Met Thr Glu Glu Glu Tyr
            1055            1060            1065
Trp Met Glu Glu Glu Gln Arg Ile Tyr Thr Arg Leu Gln Gln Glu
            1070            1075            1080
Arg Arg Glu Arg Glu Glu Ala Ile Lys Arg Lys Ala Glu Arg Asn
            1085            1090            1095
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Leu Val Ser Gln Lys His Ile Val Tyr Thr Glu Pro Leu Glu Ile
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His Ala Gly Thr Thr Ile Asp Val Leu Tyr Asn Pro Ser Asn Thr
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Val Leu Thr Gly Lys Pro Glu Val Trp Phe Arg Cys Ser Phe Asn
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Arg Trp Met Tyr Pro Gly Gly Val Leu Pro Pro Gln Lys Met Val
                1160                1165                1170

Gln Ala Glu Asn Gly Ser His Leu Lys Ala Thr Val Tyr Val Pro
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Arg Asp Ala Tyr Met Met Asp Phe Val Phe Ser Glu Ser Glu Glu
                1190                1195                1200

Gly Gly Ile Tyr Asp Asn Arg Asn Gly Leu Asp Tyr His Ile Pro
                1205                1210                1215

Val Phe Gly Ser Ile Ala Lys Glu Pro Pro Met His Ile Val His
                1220                1225                1230

Ile Ala Val Glu Met Ala Pro Ile Ala Lys Val Gly Gly Leu Gly
                1235                1240                1245

Asp Val Val Thr Ser Leu Ser Arg Ala Val Gln Asp Leu Gly His
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Asn Val Glu Val Ile Leu Pro Lys Tyr Gly Cys Leu Asn Leu Ser
                1265                1270                1275

Asn Val Lys Asn Leu Gln Ile His Gln Ser Phe Ser Trp Gly Gly
                1280                1285                1290

Ser Glu Ile Asn Val Trp Arg Gly Leu Val Glu Gly Leu Cys Val
                1295                1300                1305

Tyr Phe Leu Glu Pro Gln Asn Gly Met Phe Gly Val Gly Tyr Val
                1310                1315                1320

Tyr Gly Arg Asp Asp Asp Arg Arg Phe Gly Phe Phe Cys Arg Ser
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Ala Leu Glu Phe Leu Leu Gln Ser Gly Ser Ser Pro Asn Ile Ile
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His Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu His Lys
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Glu Asn Tyr Ala Lys Ser Ser Leu Ala Asn Ala Arg Val Val Phe
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Thr Ile His Asn Leu Glu Phe Gly Ala His His Ile Gly Lys Ala
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Met Arg Tyr Cys Asp Lys Ala Thr Thr Val Ser Asn Thr Tyr Ser
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Tyr Asn Asp Asn Phe Ile Pro Val His Tyr Thr Cys Glu Asn Val
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Val Glu Gly Lys Arg Ala Ala Lys Arg Ala Leu Gln Gln Lys Phe
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Gly Leu Gln Gln Ile Asp Val Pro Val Val Gly Ile Val Thr Arg
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Leu Thr Ala Gln Lys Gly Ile His Leu Ile Lys His Ala Ile His
                1490                1495       ·        1500

Arg Thr Leu Glu Arg Asn Gly Gln Val Val Leu Leu Gly Ser Ala
                1505                1510                1515

Pro Asp Ser Arg Ile Gln Ala Asp Phe Val Asn Leu Ala Asn Thr
                1520                1525                1530


Leu His Gly Val Asn His Gly Gln Val Arg Leu Ser Leu Thr Tyr
                1535                1540                1545

Asp Glu Pro Leu Ser His Leu Ile Tyr Ala Gly Ser Asp Phe Ile
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Leu Val Pro Ser Ile Phe Glu Pro Cys Gly Leu Thr Gln Leu Val
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Ala Met Arg Tyr Gly Thr Ile Pro Ile Val Arg Lys Thr Gly Gly
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Leu Phe Asp Thr Val Phe Asp Val Asp Asn Asp Lys Glu Arg Ala
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Arg Asp Arg Gly Leu Glu Pro Asn Gly Phe Ser Phe Asp Gly Ala
                1610                1615                1620

Asp Ser Asn Gly Val Asp Tyr Ala Leu Asn Arg Ala Ile Ser Ala
                1625                1630                1635

Trp Phe Asp Ala Arg Ser Trp Phe His Ser Leu Cys Lys Arg Val
                1640                1645                1650

Met Glu Gln Asp Trp Ser Trp Asn Arg Pro Ala Leu Asp Tyr Ile
                1655                1660                1665

Glu Leu Tyr Arg Ser Ala Ser Lys Leu
                1670
```

<210>    13
        <211>    60
        <212>    PRT
        <213>    maize
        <220>
        <221>    418..477
        <222>    REPEAT
        <223>    First 60 amino acid residue SBE-superrepeat of 180
                 amino acid repeat residue in DU1.
        <400>    13
```
Asp Gln Ser Ile Ala Gly Ser His Arg Gln Asp Gln Ser Ile Ala
```

```
        1                     5                     10                    15

Gly Ala Pro Glu Gln Ile Gln Ser Val Ala Gly Tyr Ile Lys Pro
                20                    25                    30

Asn Gln Ser Ile Val Gly Ser Cys Lys Gln His Glu Leu Ile Ile
                35                    40                    45

Pro Glu Pro Lys Lys Ile Glu Ser Ile Ile Ser Tyr Asn Glu Ile
                50                    55                    60
```

        <210>    14
        <211>    60
        <212>    PRT
        <213>    maize
        <220>
        <222>    REPEAT
        <221>    478..537
        <223>    Second 60 amino acid residue SBE-superrepeat of 180
                 amino acid repeat residue in DU1.
        <400>    14

```
Asp Gln Ser Ile Val Gly Ser His Lys Gln Asp Lys Ser Val Val
 1                    5                     10                    15

Ser Val Pro Glu Gln Ile Gln Ser Ile Val Ser His Ser Lys Pro
                20                    25                    30

Asn Gln Ser Thr Val Pro Ser Tyr Arg Gln Ala Glu Ser Ile Ile
                35                    40                    45

Gly Val Pro Glu Lys Val Gln Ser Ile Thr Ser Tyr Asp Lys Leu
                50                    55                    60
```

        <210>    15
        <211>    60
        <212>    PRT
        <213>    maize
        <220>
        <222>    REPEAT
        <221>    438..597
        <223>    Third 60 amino acid residue SBE-superrepeat of 180
                 amino acid repeat residue in DU1.
        <400>    15

```
Asp Gln Ser Ile Val Gly Ser Leu Lys Gln Asp Glu Pro Ile Ile
 1                    5                     10                    15

Ser Val Pro Glu Lys Ile Gln Ser Ile Val His Tyr Thr Lys Pro
                20                    25                    30

Asn Gln Ser Ile Val Gly Leu Pro Lys Gln Gln Gln Ser Ile Val
                35                    40                    45

His Ile Val Glu Pro Lys Gln Ser Ile Asp Gly Phe Pro Lys Gln
                50                    55                    60
```

        <210>    16
        <211>    10
        <212>    PRT
        <213>    maize
        <220>
        <221>    478..487
        <222>    REPEAT
        <223>    Sequence of SBE-repeat in DU1.
        <400>    16

```
Asp Gln Ser Ile Val Gly Ser His Lys Gln
 1                    5                     10
```

        <210>    17

```
              <211>    10
              <212>    PRT
              <213>    maize
              <220>
              <221>    538..547
              <222>    REPEAT
              <223>    Sequence of SBE-repeat in DU1.
              <400>    17
Asp Gln Ser Ile Val Gly Ser Leu Lys Gln
  1                   5                   10
              <210>    18
              <211>    10
              <212>    PRT
              <213>    maize
              <220>
              <221>    448.457
              <222>    REPEAT
              <223>    Sequence of SBE-repeat in DU1.
              <400>    18
Asn Gln Ser Ile Val Gly Ser Cys Lys Gln
  1                   5                   10

              <210>    19
              <211>    10
              <212>    PRT
              <213>    maize
              <220>
              <221>    568..577
              <222>    REPEAT
              <223>    Sequence of SBE-repeat in DU1.
              <400>    19
Asn Gln Ser Ile Val Gly Leu Pro Lys Gln
  1                   5                   10

              <210>    20
              <211>    10
              <212>    PRT
              <213>    maize
              <220>
              <221>    418..427
              <222>    REPEAT
              <223>    Sequence of SBE-repeat in DU1.
              <400>    20
Asp Gln Ser Ile Ala Gly Ser His Arg Gln
  1                   5                   10

              <210>    21
              <211>    10
              <212>    PRT
              <213>    maize
              <220>
              <221>    428..437
              <222>    REPEAT
              <223>    Sequence of SBE-repeat in DU1.
              <400>    21
Asp Gln Ser Ile Ala Gly Ala Pro Glu Gln
  1                   5                   10

              <210>    22
              <211>    10
              <212>    PRT
              <213>    maize
              <220>
              <221>    404..413
              <222>    REPEAT
              <223>    Sequence of SBE-repeat in DU1.
```

```
        <400>   22
Asp Lys Ser Ile Val Gly Val Pro Gln Gln
 1               5                   10


        <210>   23
        <211>   10
        <212>   PRT
        <213>   maize
        <220>
        <221>   598..607
        <222>   REPEAT
        <223>   Sequence of SBE-repeat in DU1.
        <400>   23
Asp Leu Ser Ile Val Gly Asn Glu Phe Gln
 1               5                   10


        <210>   24
        <211>   25
        <212>   PRT
        <213>   maize
        <220>
        <221>   529..553
        <222>   REPEAT
        <223>   Conserved M-box sequence in maize SBEI.
        <400>   24
Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly
 1               5                   10                  15

Asp Lys Thr Ile Ala Phe Leu Leu Met Asp
                20                  25


        <210>   25
        <211>   25
        <212>   PRT
        <213>   pea
        <220>
        <221>   529..553
        <222>   REPEAT
        <223>   Conserved M-box sequence in pea SBEII.
        <400>   25
Lys Cys Val Ser Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly
 1               5                   10                  15

Asp Lys Thr Ile Ala Phe Leu Leu Met Asp
                20                  25


        <210>   26
        <211>   25
        <212>   PRT
        <213>   wheat
        <220>
        <221>   529..553
        <222>   REPEAT
        <223>   Conserved M-box sequence in wheat SBEI.
        <400>   26
Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly
 1               5                   10                  15

Asp Lys Thr Met Ala Phe Leu Leu Met Asp
                20                  25


        <210>   27
        <211>   25
        <212>   PRT
        <213>   maize
        <220>
```

```
        <221>    572..596
        <222>    REPEAT
        <223>    Conserved M-box sequence in maize SBEIa.
        <400>    27
Lys Cys Val Thr Tyr Cys Glu Ser His Asp Gln Ala Leu Val Gly
 1                5                   10                  15

Asp Lys Thr Ile Ala Phe Trp Leu Met Asp
                20                  25


        <210>    28
        <211>    15
        <212>    PRT
        <213>    maize
        <220>
        <221>    572..596
        <222>    REPEAT
        <223>    Conserved M-box sequence in maize SBEIIb.
        <400>    28
Lys Cys Val Thr Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly
 1                5                   10                  15


        <210>    29
        <211>    25
        <212>    PRT
        <213>    pea
        <220>
        <221>    572..596
        <222>    REPEAT
        <223>    Conserved M-box sequence in pea SBEI.
        <400>    29
Lys Cys Val Val Tyr Cys Glu Ser His Asp Gln Ala Leu Val Gly
 1                5                   10                  15
Asp Lys Thr Met Ala Phe Leu Leu Met Asp
                20                  25


        <210>    30
        <211>    25
        <212>    PRT
        <213>    yeast
        <220>
        <221>    477..501
        <222>    REPEAT
        <223>    Conserved M-box sequence in yeast GLC3 glycogen
                 synthase.
        <400>    30
Lys Val Val Ala Tyr Cys Glu Ser His Asp Gln Ala Leu Val Gly
 1                5                   10                  15
Asp Lys Ser Leu Ala Phe Trp Leu Met Asp
                20                  25


        <210>    31
        <211>    25
        <212>    PRT
        <213>    Homo sapiens
        <220>
        <221>    477..501
        <222>    REPEAT
        <223>    Conserved M-box sequence in human liver glycogen
                 synthase.
        <400>    31
Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly
 1                5                   10                  15

Asp Lys Thr Leu Ala Phe Trp Leu Met Asp
                20                  25
```

```
                 <210>    32
                 <211>    28
                 <212>    PRT
                 <213>    maize
                 <220>
                 <221>    150..177
                 <222>    REPEAT
                 <223>    Second 28 amino acid residue repeat of 85 residue
                          repeat in N-terminus of DU1.
                 <400>    32
Glu Thr Val Asp Glu Ala Glu Val Glu Glu Asp Lys Phe Glu Val
1                5                   10                  15

Asp Thr Ser Gly Ile Val Leu Arg Asn Val Ala Val Arg
                20                  25


                 <210>    33
                 <211>    29
                 <212>    PRT
                 <213>    artificial sequence
                 <220>
                 <221>    178..205
                 <222>    REPEAT
                 <223>    Second 28 amino acid residue repeat of 85 residue
                          repeat in N-terminus of DU1.
                 <400>    33
Glu Val Asp Pro Lys Asp Glu His Asn Ala Lys Asp Val Phe Val
1                5                   10                  15

Val Asp Ser Ser Gly Thr Ala Pro Asp Asn Ala Ala Val Glu
                20                  25


                 <210>    34
                 <211>    27
                 <212>    PRT
                 <213>    maize
                 <220>
                 <221>    206..233
                 <222>    REPEAT
                 <223>    Third 28 amino acid residue repeat of 85 residue
                          repeat in N-terminus of DU1.
                 <400>    34
Glu Val Val Asp Glu Ala Glu Val Glu Glu Asp Met Val Asp Val
1                5                   10                  15

Asp Ile Leu Gly Leu Asp Leu Asn Asn Ala Thr Ile
                20                  25
                 <210>    35
                 <211>    1230
                 <212>    PRT
                 <213>    potato
                 <220>
                 <223>    Deduced amino acid sequence of potato starch synthase
                          SSIII.
                 <400>    35
Met Asp Val Pro Phe Pro Leu His Arg Ser Leu Ser Cys Thr Ser
1                5                   10                  15
Val Ser Asn Ala Ile Thr His Leu Lys Ile Lys Pro Ile Leu Gly
                20                  25                  30

Phe Val Ser His Gly Thr Thr Ser Leu Ser Val Gln Ser Ser Ser
                35                  40                  45

Trp Arg Lys Asp Gly Met Val Thr Gly Val Ser Phe Ser Ile Cys
                50                  55                  60
```

```
Ala Asn Phe Ser Gly Arg Arg Arg Arg Lys Val Ser Thr Pro Arg
                65                  70              75

Ser Gln Gly Ser Ser Pro Lys Gly Phe Val Pro Arg Lys Pro Ser
                80              85              90

Gly Met Ser Thr Gln Arg Lys Val Gln Lys Ser Asn Gly Asp Lys
                95          100             105

Glu Ser Lys Ser Thr Ser Thr Ser Lys Glu Ser Glu Ile Ser Asn
                110             115             120

Gln Lys Thr Val Glu Ala Arg Val Glu Thr Ser Asp Asp Asp Thr
                125             130             135

Lys Gly Val Val Arg Asp His Lys Phe Leu Glu Asp Glu Asp Glu
                140             145             150

Ile Asn Gly Ser Thr Lys Ser Ile Ser Met Ser Pro Val Arg Val
                155             160             165

Ser Ser Gln Phe Val Glu Ser Glu Glu Thr Gly Gly Asp Asp Lys
                170             175             180

Asp Ala Val Lys Leu Asn Lys Ser Lys Arg Ser Glu Glu Ser Gly
                185             190             195

Phe Ile Ile Asp Ser Val Ile Arg Glu Gln Ser Gly Ser Gln Gly
                200             205             210

Glu Thr Asn Ala Ser Ser Lys Gly Ser His Ala Val Gly Thr Lys
                215             220             225

Leu Tyr Glu Ile Leu Gln Val Asp Val Glu Pro Gln Gln Leu Lys
                230             235             240

Glu Asn Asn Ala Gly Asn Val Glu Tyr Lys Gly Pro Val Ala Ser
                245             250             255

Lys Leu Leu Glu Ile Thr Lys Ala Ser Asp Val Glu His Thr Glu
                260             265             270

Ser Asn Glu Ile Asp Asp Leu Asp Thr Asn Ser Phe Phe Lys Ser
                275             280             285

Asp Leu Ile Glu Glu Asp Glu Pro Leu Ala Ala Gly Thr Val Glu
                290             295             300

Thr Gly Asp Ser Ser Leu Asn Leu Arg Leu Glu Met Glu Ala Asn
                305             310             315

Leu Arg Arg Gln Ala Ile Glu Arg Leu Ala Glu Glu Asn Leu Leu
                320             325             330

Gln Gly Ile Arg Leu Phe Cys Phe Pro Glu Val Val Lys Pro Asp
                335             340             345

Glu Asp Val Glu Ile Phe Leu Asn Arg Gly Leu Ser Thr Leu Lys
                350             355             360

Asn Glu Ser Asp Val Leu Ile Met Gly Ala Phe Asn Glu Trp Arg
                365             370             375
```

```
Tyr Arg Ser Phe Thr Thr Arg Leu Thr Glu Thr His Leu Asn Gly
              380             385                     390

Asp Trp Trp Ser Cys Lys Ile His Val Pro Lys Glu Ala Tyr Arg
              395             400                     405

Ala Asp Phe Val Phe Phe Asn Gly Gln Asp Val Tyr Asp Asn Asn
              410             415                     420

Asp Gly Asn Asp Phe Ser Ile Thr Val Lys Gly Gly Met Gln Ile
              425             430                     435

Ile Asp Phe Glu Asn Phe Leu Leu Glu Glu Lys Trp Arg Glu Gln
              440             445                     450

Glu Lys Leu Ala Lys Glu Gln Ala Glu Arg Glu Arg Leu Ala Glu
              455             460                     465

Glu Gln Arg Arg Ile Glu Ala Glu Lys Ala Glu Ile Glu Ala Asp
              470             475                     480

Arg Ala Gln Ala Lys Glu Glu Ala Ala Lys Lys Lys Lys Val Leu
              485             490                     495

Arg Glu Leu Met Val Lys Ala Thr Lys Thr Arg Asp Ile Thr Trp
              500             505                     510

Tyr Ile Glu Pro Ser Glu Phe Lys Cys Glu Asp Lys Val Arg Leu
              515             520                     525

Tyr Tyr Asn Lys Ser Ser Gly Pro Leu Ser His Ala Lys Asp Leu
              530             535                     540

Trp Ile His Gly Gly Tyr Asn Asn Trp Lys Asp Gly Leu Ser Ile
              545             550                     555


Val Lys Lys Leu Val Lys Ser Glu Arg Ile Asp Gly Asp Trp Trp
              560             565                     570

Tyr Thr Glu Val Val Ile Pro Asp Gln Ala Leu Phe Leu Asp Trp
              575             580                     585

Val Phe Ala Asp Gly Pro Pro Lys His Ala Ile Ala Tyr Asp Asn
              590             595                     600

Asn His Arg Gln Asp Phe His Ala Ile Val Pro Asn His Ile Pro
              605             610                     615

Glu Glu Leu Tyr Trp Val Glu Glu Glu His Gln Ile Phe Lys Thr
              620             625                     630

Leu Gln Glu Glu Arg Arg Leu Arg Glu Ala Ala Met Arg Ala Lys
              635             640                     645

Val Glu Lys Thr Ala Leu Leu Lys Thr Glu Thr Lys Glu Arg Thr
              650             655                     660

Met Lys Ser Phe Leu Leu Ser Gln Lys His Val Val Tyr Thr Glu
              665             670                     675

Pro Leu Asp Ile Gln Ala Gly Ser Ser Val Thr Val Tyr Tyr Asn
              680             685                     690

Pro Ala Asn Thr Val Leu Asn Gly Lys Pro Glu Ile Trp Phe Arg
              695             700                     705
```

```
Cys Ser Phe Asn Arg Trp Thr His Arg Leu Gly Pro Leu Pro Pro
                710                 715                 720

Gln Lys Met Ser Pro Ala Glu Asn Gly Thr His Val Arg Ala Thr
                725                 730                 735


Val Lys Val Pro Leu Asp Ala Tyr Met Met Asp Phe Val Phe Ser
                740                 745                 750

Glu Arg Glu Asp Gly Gly Ile Phe Asp Asn Lys Ser Gly Met Asp
                755                 760                 765

Tyr His Ile Pro Val Phe Gly Gly Val Ala Lys Glu Pro Pro Met
                770                 775                 780

His Ile Val His Ile Ala Val Glu Met Ala Pro Ile Ala Lys Val
                785                 790                 795

Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala Val Gln
                800                 805                 810

Asp Leu Asn His Asn Val Asp Ile Ile Leu Pro Lys Tyr Asp Cys
                815                 820                 825

Leu Lys Met Asn Asn Val Lys Asp Phe Arg Phe His Lys Asn Tyr
                830                 835                 840

Phe Trp Gly Gly Thr Glu Ile Lys Val Trp Phe Gly Lys Val Glu
                845                 850                 855

Gly Leu Ser Val Tyr Phe Leu Glu Pro Gln Asn Gly Leu Phe Ser
                860                 865                 870

Lys Gly Cys Val Tyr Gly Cys Ser Asn Asp Gly Glu Arg Phe Gly
                875                 880                 885

Phe Phe Cys His Ala Ala Leu Glu Phe Leu Leu Gln Gly Gly Phe
                890                 895                 900

Ser Pro Asp Ile Ile His Cys His Asp Trp Ser Ser Ala Pro Val
                905                 910                 915


Ala Trp Leu Phe Lys Glu Gln Tyr Thr His Tyr Gly Leu Ser Lys
                920                 925                 930

Ser Arg Ile Val Phe Thr Ile His Asn Leu Glu Phe Gly Ala Asp
                935                 940                 945

Leu Ile Gly Arg Ala Met Thr Asn Ala Asp Lys Ala Thr Thr Val
                950                 955                 960

Ser Pro Thr Tyr Ser Gln Glu Val Ser Gly Asn Pro Val Ile Ala
                965                 970                 975

Pro His Leu His Lys Phe His Gly Ile Val Asn Gly Ile Asp Pro
                980                 985                 990

Asp Ile Trp Asp Pro Leu Asn Asp Lys Phe Ile Pro Ile Pro Tyr
                995                 1000                1005

Thr Ser Glu Asn Val Val Glu Gly Lys Thr Ala Ala Lys Glu Ala
                1010                1015                1020
```

```
Leu Gln Arg Lys Leu Gly Leu Lys Gln Ala Asp Leu Pro Leu Val
            1025            1030            .        1035

Gly Ile Ile Thr Arg Leu Thr His Gln Lys Gly Ile His Leu Ile
            1040            1045            1050

Lys His Ala Ile Trp Arg Thr Leu Glu Arg Asn Gly Gln Val Val
            1055            1060            1065

Leu Leu Gly Ser Ala Pro Asp Pro Arg Val Gln Asn Asn Phe Val
            1070            1075            1080

Asn Leu Ala Asn Gln Leu His Ser Lys Tyr Asn Asp Arg Ala Arg
            1085             . 1090            1095


Leu Cys Leu Thr Tyr Asp Glu Pro Leu Ser His Leu Ile Tyr Ala
            1100            1105            1110

Gly Ala Asp Phe Ile Leu Val Pro Ser Ile Phe Glu Pro Cys Gly
            1115            1120            1125

Leu Thr Gln Leu Thr Ala Met Arg Tyr Gly Ser Ile Pro Val Val
            1130            1135            1140

Arg Lys Thr Gly Gly Leu Tyr Asp Thr Val Phe Asp Val Asp His
            1145            1150            1155

Asp Lys Glu Arg Ala Gln Gln Cys Gly Leu Glu Pro Asn Gly Phe
            1160            1165            1170

Ser Phe Asp Gly Ala Asp Ala Gly Gly Val Asp Tyr Ala Leu Asn
            1175            1180            1185

Arg Ala Leu Ser Ala Trp Tyr Asp Gly Arg Asp Trp Phe Asn Ser
            1190            1195            1200

Leu Cys Lys Gln Val Met Glu Gln Asp Trp Ser Trp Asn Arg Pro
            1205            1210            1215

Ala Leu Asp Tyr Leu Glu Leu Tyr His Ala Ala Arg Lys Leu Glu
            1220            1225            1230
```

```
        <210>   36
        <211>   9
        <212>   DNA
        <213>   artificial sequence
        <220>
        <222>   repeat_unit
        <223>   Sequence of the nine base pair direct repeats flanking
                a Mu1 element in cloned fragment.
        <400>   36
gtgagaatg                       9


        <210>   37
        <211>   32
        <212>   DNA
        <213>   artificial sequence
        <221>   primer
        <223>   Primer containing restriction sites
        <400>   37
aaacccgggaattcgatggagatggtcctacg                        32
```